

1/2/02

A-378CIP5.ST25.txt
SEQUENCE LISTING

<110> BOYLE, WILLIAM J.
LACEY, DAVID LEE
CALZONE, FRANK J.
CHANG, MING-SHI
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

<130> A-378CIP5

<140> US 09/613,591
<141> 2000-07-10

<150> US 09/457,647
<151> 1999-12-09

<150> US 09/350,670
<151> 1999-07-09

<150> US 08/706,945
<151> 1996-09-03

<150> US 08/577,788
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A-378CIP5.ST25.txt

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A-378CIP5.ST25.txt

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A-378CIP5.ST25.txt

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A-378CIP5.ST25.txt

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gcctccacc gcccgtcctg cggcggtat ttgacggtcc gtagttaat tcgtcttccg 240
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atacaagtat gtgcgtacat ttttatttga tagatatac aacagaaaga gacttacacg 660
ttttgattcg taaggcttcg gtaataatcg tcatacttat cccttgatt tgggtcacta 720
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A-378CIP5.ST25.txt

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tggaaagtga ccgtgcgcctt actacagcct aatattttg aaatatccca agagctttt 480
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A-378CIP5.ST25.txt

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A-378CIP5.ST25.txt

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gcctcccacc gcccgtcccg cggcggtat ttgacggcc gtagttat tcgtttccg		240
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taagttata cctgcagagt attaaaaatt tttaagtaa actgtttacg attttaaagaa		360

A-378CIP5.ST25.txt

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A-378CIP5.ST25.txt

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Gly Thr Tyr

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A-378CIP5.ST25.txt

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A-378CIP5.ST25.txt

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<213> Homo sapiens

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gttctcctat taatgaaata tcttcattat gatgaagaaa ctt 43

<210> 78
<211> 40
<212> DNA

A-378CIP5.ST25.txt

<213> Homo sapiens
<400> 78
tacgcactgg atccttataa gcagcttatt tttactgatt 40

<210> 79
<211> 40
<212> DNA
<213> Mus musculus

<400> 79
gttctccctca tatggaaaact ctgcctccaa aataacctgca 40

<210> 80
<211> 43
<212> DNA
<213> Mus musculus

<400> 80
tacgcactgg atccttatgt tgcatttcct ttctgaatta gca 43

<210> 81
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 81
ccggaaacag ataatgag 18

<210> 82
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 82
gatcctcatt atctgttt 18

<210> 83
<211> 30
<212> DNA
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<220>
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<400> 83
ccggaaacag agaagccacg caaaagtaag 30

<210> 84
<211> 30
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<220>
<223> pAMG21

A-378CIP5.ST25.txt

<400> 84
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<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 85
tatgttaatg ag 12

<210> 86
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 86
gatcctcatt aaca 14

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 87
tatgttccgg aaacagttaa g 21

<210> 88
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 88
gatccttaac tgtttccgga aca 23

<210> 89
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 89
tatgttccgg aaacagtgaa tcaactcaaa aataag 36

<210> 90
<211> 38
<212> DNA
<213> Artificial Sequence

A-378CIP5.ST25.txt

<220>
<223> pAMG21

<400> 90
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<210> 91
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21

<400> 91
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ctggtcatca gctgctgtgt cataaatgtg ctccgggtac 100

<210> 92
<211> 92
<212> DNA
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<220>
<223> pAMG21

<400> 92
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ttggaggcag agtttcttg tcgtcgctgt cg 92

<210> 93
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21-huOPG

<400> 93
acaaacacaaa tcgatttgat actaga 26

<210> 94
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21-huOPG

<400> 94
tttgttttaa ctaattaaag gaggaataaa atatgagagg atcgcatcac 50

<210> 95
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21-huOPG

A-378CIP5.ST25.txt

<400> 95	catcaccatc acgaaacctt cccggcgaaa tacctgcact acgacgaaga	50
<210> 96		
<211> 49		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> pAMG21-huOPG		
<400> 96	aacctccac cagctgctgt gcgacaaatg cccggcggtt acccaaaca	49
<210> 97		
<211> 26		
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<223> pAMG21-huOPG		
<400> 97	tgtttggta cccggcggtt atttgt	26
<210> 98		
<211> 50		
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<210> 99		
<211> 49		
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<210> 100		
<211> 50		
<212> DNA		
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<212> DNA		
<213> Homo sapiens		

<400> 101	acaaaacacaaa tcgatttgat actagattt ttttaactaa tttaaggagg aataaaaatg	59
<210> 102		
<211> 48		
<212> DNA		
<213> Homo sapiens		
<400> 102	ctaattaaag gaggaataaaa atgaaagaaaa cttttcctcc aaaatatc	48
<210> 103		
<211> 31		
<212> DNA		
<213> Homo sapiens		
<400> 103	tgttgggta cccggcggac atttatcaca c	31
<210> 104		
<211> 59		
<212> DNA		
<213> Homo sapiens		
<400> 104	acaaaacacaaa tcgatttgat actagattt ttttaactaa tttaaggagg aataaaaatg	59
<210> 105		
<211> 54		
<212> DNA		
<213> Homo sapiens		
<400> 105	ctaattaaag gaggaataaaa atgaaaaaaaaa aagaaaacttt tcctccaaaaa tatc	54
<210> 106		
<211> 31		
<212> DNA		
<213> Homo sapiens		
<400> 106	tgttgggta cccggcggac atttatcaca c	31
<210> 107		
<211> 44		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> PCR primer for Fc-hOPG fusion protein.		
<400> 107	cagccccgggt aaaatggaaa cgtttcctcc aaaatatctt catt	44
<210> 108		
<211> 44		
<212> DNA		
<213> Artificial Sequence		

<220>

A-378CIP5.ST25.txt

<223> PCR primer for FchOPG fusion protein.

<400> 108
cgtttccatt ttacccgggc tgagcgagag gctcttctgc gtgt

44

<210> 109
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc/muOPG

<400> 109
cgctcagccc gggtaaaatg gaaacgttgc ctccaaaata cctgc

45

<210> 110
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc/muOPG

<400> 110
ccattttacc cgggctgagc gagaggctct tctgcgtgt

39

<210> 111
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 111
gaaaataaga tgcttagctg cagctgaacc aaaatc

36

<210> 112
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> muOPG

<400> 112
cagctgcagc taagcagctt atttcacgg attg

34

<210> 113
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 113
aaaaataagc tgcttagctg cagctgaacc aaaatc

36

<210> 114
<211> 35

A-378CIP5.ST25.txt

<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 114
cagctgcagc taagcagctt attttactg attgg 35

<210> 115
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> pAMG21-huOPG

<220>
<221> misc_feature
<223> Linker with XbaI and KpnI sites inserted into human sequence.

<400> 115
ctagaaggag gaataacata tggaaacttt tgctccaaaa tatcttcatt atgatgaaga 60
aactagtcat cagctgctgt gtgataaaatg tccgccccgt ac 102

<210> 116
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 116
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ttggagcaaa agttccata tgttattcct cctt 94

<210> 117
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 117
ctagaaggag gaataacata tggaaacttt tcctgctaaa tatcttcatt atgatgaaga 60
aa 62

<210> 118
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 118
ctagtttctt catcataatg aagatatttgcaggaaaag tttccatatgttattcctcc 60

tt
<210> 119
<211> 51
<212> PRT
<213> Homo sapiens

<400> 119

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met
1 5 10 15

Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg
20 25 30

Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
35 40 45

Asp Trp His
50

<210> 120
<211> 2432
<212> DNA
<213> Rattus rattus

<220>
<221> CDS
<222> (124)..(1326)
<223>

<400> 120
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ggcagcagag aagcacctag cactggccca gcggctgccc cctgagggtt ccagaggacc 120
aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc 168
Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile
1 5 10 15
att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216
Ile Glu Trp Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr
20 25 30
gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264
Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly
35 40 45
acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 312
Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val
50 55 60
cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 360
Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu
65 70 75
tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 408
Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln
80 85 90 95
gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 456
Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg

A-378CIP5.ST25.txt

100

105

110

tac	ctg	gag	ctc	gaa	ttc	tgc	ttg	aag	cac	cg	agc	tgt	ccc	cca	ggc	504
Tyr	Leu	Glu	Leu	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	
115								120					125			
ttg	gg	gt	ctg	cag	gct	ggg	acc	cca	gag	cga	aac	acg	gtt	tgc	aaa	552
Leu	Gly	Val	Leu	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	
130							135					140				
aga	tgt	ccg	gat	ggg	ttc	ttc	tca	gg	gag	acg	tca	tcg	aaa	gca	ccc	600
Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	
145							150					155				
tgt	agg	aaa	cac	acc	aac	tgc	agc	tca	ctt	ggc	ctc	ctg	cta	att	cag	648
Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Ser	Leu	Gly	Leu	Leu	Leu	Ile	Gln	
160							165				170			175		
aaa	gga	aat	gca	aca	cat	gac	aat	gta	tgt	tcc	gga	aac	aga	gaa	gca	696
Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	
180							185					190				
act	caa	aat	tgt	gaa	ata	gat	gtc	acc	ctg	tgc	gaa	gag	gca	ttc	ttc	744
Thr	Gln	Asn	Cys	Glu	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	
195							200					205				
agg	ttt	gct	gt	cct	acc	aag	att	ata	ccg	aat	tgg	ctg	agt	gtt	ctg	792
Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	
210							215					220				
gtg	gac	agt	ttg	cct	ggg	acc	aaa	gt	aat	gca	gag	agt	gta	gag	agg	840
Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	
225							230					235				
ata	aaa	cgg	aga	cac	agc	tcg	caa	gag	caa	act	ttc	cag	cta	ctt	aag	888
Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	
240							245					250			255	
ctg	tgg	aag	cat	caa	aac	aga	gac	cag	gaa	atg	gt	aag	aag	atc	atc	936
Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	
260							265					270				
caa	gac	att	gac	ctc	tgt	gaa	agc	agt	gt	caa	cgg	cat	atc	ggc	cac	984
Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Ile	Gly	His	
275							280					285				
gcg	aac	ctc	acc	aca	gag	cag	ctc	cgc	atc	ttg	atg	gag	agc	ttg	cct	1032
Ala	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Arg	Ile	Leu	Met	Glu	Ser	Leu	Pro	
290							295					300				
ggg	aag	aag	atc	agc	cca	gac	gag	att	gag	aga	acg	aga	aag	acc	tgc	1080
Gly	Lys	Lys	Ile	Ser	Pro	Asp	Glu	Ile	Glu	Arg	Thr	Arg	Lys	Thr	Cys	
305							310					315				
aaa	ccc	agc	gag	cag	ctc	ctg	aag	cta	ctg	agc	ttg	tgg	agg	atc	aaa	1128
Lys	Pro	Ser	Glu	Gln	Leu	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	
320							325					330			335	
aat	gga	gac	caa	gac	acc	ttg	aag	ggc	ctg	atg	tac	gca	ctc	aag	cac	1176
Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His	
340							345					350				
ttg	aaa	gca	tac	cac	ttt	ccc	aaa	acc	gtc	acc	cac	agt	ctg	agg	aag	1224
Leu	Lys	Ala	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	His	Ser	Leu	Arg	Lys	
355							360					365				
acc	atc	agg	ttc	ttg	cac	agc	ttc	acc	atg	tac	cga	ttg	tat	cag	aaa	1272
Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Arg	Leu	Tyr	Gln	Lys	

A-378CIP5.ST25.txt

370

375

380

ctc ttt cta gaa atg ata ggg aat cag gtt caa tca gtg aag ata agc Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser	1320
385 390 395	
tgc tta tagtttagaa tggtcactgg gctgtttctt caggatgggc caacactgat Cys Leu	1376
400	
ggagcagatg gctgcttc tcggctttga aatggcagtt gattccttc tcatacgatg gtggaaatga agatcctcca gcccaacaca cacactgggg agtctgagtc aggagagtga	1436 1496
ggcaggctat ttgataattg tgcaaagctg ccaggtgtac acctagaaag tcaaggcaccc tgagaaagag gatattttta taacctcaaa cataggccct ttccttcctc tccttatgga	1556 1616
tgagtaactca gaaggcttct actatcttct gtgtcatccc tagatgaagg cctctttat ttatTTTTT attcttttt tcggagctgg ggaccgaacc cagggccttg cgcttgcgag	1676 1736
gcaagtgctc taccactgag ctaaatctcc aaccctgaa ggctcttcc tttctgcctc tgatagtcta tgacattctt tttctacaa ttcgtatcag gtgcacgagc cttatccat	1796 1856
ttgttaggTTT ctaggcaagt tgaccgttag ctatTTTCC ctctgaagat ttgattcgag ttgcagactt ggctagacaa gcagggtag gttatggtag tttatTTAac agactgccac	1916 1976
caggagtcca gtgttcttg ttccctctgta gttgtaccta agctgactcc aagtacattt agtatgaaaa ataatcaaca aattttattc cttctatcaa cattggctag ctttgtttca	2036 2096
gggcactaaa agaaaactact atatggagaa agaattgata ttgccccaa cgttcaacaa cccaatagtt tatccagctg tcatgcctgg ttcaagtgtct actgactatg cggcccttta	2156 2216
ttactgcatg cagtaattca actggaaata gtaataataa taatagaaaat aaaatctaga ctccattgga tctctctgaa tatggaaata tctaacttaa gaagcttga gatttcagtt	2276 2336
gtgttaaagg cttttattaa aaagctgatg ctcttctgta aaagttacta atatatctgt aagactatta cagttattgct atttatatcc atccag	2396 2432

<210> 121

<211> 401

<212> PRT

<213> Rattus rattus

<400> 121

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile	
1 5 10 15	

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp	
20 25 30	

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr	
35 40 45	

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro	
50 55 60	

A-378CIP5.ST25.txt

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305 310 315 320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
 340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
 370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 385 390 395 400

Leu

<210> 122
 <211> 1325
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (91)..(1293)
 <223>

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> At position 11, R is a purine.

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gctgcctcct gaggtttccc gaggaccaca atg aac aag tgg ctg tgc tgc gca	114
Met Asn Lys Trp Leu Cys Cys Ala	
1 5	
ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt	162
Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu	
10 15 20	
ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg	210
Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu	
25 30 35 40	
tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg	258
Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val	
45 50 55	
agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac	306
Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp	
60 65 70	
agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag	354
Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys	
75 80 85	
gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg	402
Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val	

A-378CIP5.ST25.txt

90

95

100

tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag	450
Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
105 110 115 120	
cac cgg agc tgt ccc ccg ggc tcc ggc gtg gtg caa gct gga acc cca	498
His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala Gly Thr Pro	
125 130 135	
gag cga aac aca gtt tgc aaa aaa tgt cca gat ggg ttc ttc tca ggt	546
Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe Phe Ser Gly	
140 145 150	
gag act tca tcg aaa gca ccc tgt ata aaa cac acg aac tgc agc aca	594
Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn Cys Ser Thr	
155 160 165	
ttt ggc ctc ctg cta att cag aaa gga aat gca aca cat gac aac tgt	642
Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His Asp Asn Cys	
170 175 180	
tgt tcc gga aac aga gaa gcc acg caa aag tgt gga ata gat gtc acc	690
Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile Asp Val Thr	
185 190 195 200	
ctg tgt gaa gag gcc ttc ttc agg ttt gct gtt cct acc aag att ata	738
Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Ile Ile	
205 210 215	
cca aat tgg ctg agt gtt ttg gtg gac agt ttg cct ggg acc aaa gtg	786
Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly Thr Lys Val	
220 225 230	
aat gcc gag agt gta gag agg ata aaa cgg aga cac agc tca caa gag	834
Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser Ser Gln Glu	
235 240 245	
caa acc ttc cag ctg ctg aag ctg tgg aaa cat caa aac aga gac cag	882
Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Arg Asp Gln	
250 255 260	
gaa atg gtg aag aag atc atc caa gac att gac ctc tgt gaa agc agc	930
Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Ser Ser	
265 270 275 280	
gtg cag cgg cat ctc ggc cac tcg aac ctc acc aca gag cag ctt ctt	978
Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu Gln Leu Leu	
285 290 295	
gcc ttg atg gag agc ctg cct ggg aag aag atc agc cca gaa gag att	1026
Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro Glu Glu Ile	
300 305 310	
gag aga acg aga aag acc tgc aaa tcg agc gag cag ctc ctg aag cta	1074
Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu Leu Lys Leu	
315 320 325	
ctc agt tta tgg agg atc aaa aat ggt gac caa gac acc ttg aag ggc	1122
Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly	
330 335 340	
ctg atg tat gcc ctc aag cac ttg aaa aca tcc cac ttt ccc aaa act	1170
Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe Pro Lys Thr	
345 350 355 360	
gtc acc cac agt ctg agg aag acc atg agg ttc ctg cac agc ttc aca	1218
Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His Ser Phe Thr	

A-378CIP5.ST25.txt

365

370

375

atg tac aga ctg tat cag aag ctc ttt tta gaa atg ata ggg aat cag	1266										
Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln											
380	385		390	gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg	1313	Val Gln Ser Val Lys Ile Ser Cys Leu		395	400	gctgtttctt ca	1325
	390										
gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg	1313										
Val Gln Ser Val Lys Ile Ser Cys Leu											
395	400										
gctgtttctt ca	1325										

<210> 123
 <211> 401
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> At position 11, R is a purine.

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile					
1	5		10		15
	10		15		
	15				

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp			
20	25		30
	30		

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr			
35	40		45
	45		

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro			
50	55		60
	60		

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys					
65	70		75		80
	75		80		
	80				

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu			
85	90		95
	95		

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr			
100	105		110
	110		

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser			
115	120		125
	125		

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys			
130	135		140
	140		

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys					
145	150		155		160
	155		160		
	160				

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys			
165	170		175
	175		

A-378CIP5.ST25.txt

Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser
275 280 285

Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
305 310 315 320

Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
340 345 350

Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
355 360 365

Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 124
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (95) .. (1297)
 <223>

<220>
 <221> misc_feature
 <222> (63) .. (63)
 <223> At position 63, Y is a pyrimidine.

<400> 124	gtatatataa cgtgatgagc gtacgggtgc ggagacgcac cggcgcgctc gcccagccgc	60
cgyc	ctccaag cccctgaggt ttccggggac caca atg aac aag ttg ctg tgc tgc	115
	Met Asn Lys Leu Leu Cys Cys	
	1 5	
gcg ctc	gtg ttt ctg gac atc tcc att aag tgg acc acc cag gaa acg	163
Ala Leu Val	Phe Leu Asp Ile Ser Ile Lys Trp Thr Gln Glu Thr	
10	15 20	
ttt cct	cca aag tac ctt cat tat gac gaa gaa acc tct cat cag ctg	211
Phe Pro	Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu	
25	30 35	
ttg tgt	gac aaa tgt cct cct ggt acc tac cta aaa caa cac tgt aca	259
Leu Cys Asp	Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr	
40	45 50 55	
gca aag	tgg aag tcc gtg tgc gcc cct tgc cct gac cac tac tac aca	307
Ala Lys Trp	Lys Ser Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr	
60	65 70	
gac agc	tgg cac acc agt gac gag tgt cta tac tgc agc ccc gtg tgc	355
Asp Ser Trp	His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys	
75	80 85	
aag gag	ctg cag tac gtc aag cag gag tgc aat cgc acc cac aac cgc	403
Lys Glu Leu	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg	
90	95 100	
gtg tgc	gaa tgc aag gaa ggg cgc tac ctt gag ata gag ttc tgc ttg	451
Val Cys Glu	Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu	
105	110 115	
aaa cat	agg agc tgc cct cct gga ttt gga gtg gtg caa gct gga acc	499
Lys His Arg	Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
120	125 130 135	
cca gag	cga aat aca gtt tgc aaa aga tgt cca gat ggg ttc ttc tca	547
Pro Glu Arg	Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser	
140	145 150	
aat gag	acg tca tct aaa gca ccc tgt aga aaa cac aca aat tgc agt	595
Asn Glu Thr	Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser	
155	160 165	
gtc ttt	ggg ctc ctg cta act cag aaa gga aat gca aca cac gac aac	643
Val Phe	Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn	
170	175 180	
ata tgt	tcc gga aac agt gaa tca act caa aaa tgt gga ata gat gtt	691
Ile Cys Ser	Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val	
185	190 195	
acc ctg	tgt gag gag gca ttc ttc agg ttt gct gtt cct aca aag ttt	739
Thr Leu	Cys Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe	
200	205 210 215	

A-378CIP5.ST25.txt

acg cct aac tgg ctt agt gtc ttg gta gac aat ttg cct ggc acc aaa	787
Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys	
220 225 230	
gta aac gca gag agt gta gag agg ata aaa cgg caa cac agc tca caa	835
Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln	
235 240 245	
gaa cag act ttc cag ctg ctg aag tta tgg aaa cat caa aac aaa gcc	883
Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala	
250 255 260	
caa gat ata gtc aag aag atc atc caa gat att gac ctc tgt gaa aac	931
Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn	
265 270 275	
agc gtg cag cgg cac att gga cat gct aac ctc acc ttc gag cag ctt	979
Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu	
280 285 290 295	
cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga gca gaa gac	1027
Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp	
300 305 310	
att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag atc ctg aag	1075
Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys	
315 320 325	
ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac acc ttg aag	1123
Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys	
330 335 340	
ggc cta atg cac gca cta aag cac tca aag acg tac cac ttt ccc aaa	1171
Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys	
345 350 355	
act gtc act cag agt cta aag aag acc atc agg ttc ctt cac agc ttc	1219
Thr Val Thr Gln Ser Leu Lys Thr Ile Arg Phe Leu His Ser Phe	
360 365 370 375	
aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg ata ggt aac	1267
Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn	
380 385 390	
cag gtc caa tca gta aaa ata agc tgc tta taactggaaa tggccattga	1317
Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
395 400	
gctgttcct cacaattggc gagatccat ggatgataa	1356

<210> 125
<211> 401
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (63)..(63)
<223> At position 63, Y is a pyrimidine.

<400> 125

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
1 5 10 15

A-378CIP5.ST25.txt

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln
260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
275 280 285

A-378CIP5.ST25.txt

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

<210> 126
<211> 139
<212> PRT
<213> Homo sapiens

<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys
1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala
35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys
50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly
Page 34

A-378CIP5.ST25.txt
115 120 125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys
130 135

<210> 127
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> huOPG

<400> 127
acctacttct ttgaagagta gtcgacgaca cactatttac aggccggcc 48

<210> 128
<211> 219
<212> PRT
<213> Rattus rattus

<400> 128

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165 170 175

Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
210 215

<210> 129
<211> 281
<212> PRT
<213> Rattus rattus

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Thr Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr
65 70 75 80

Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
85 90 95

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln
100 105 110

Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys
115 120 125

Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys
130 135 140

Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln
145 150 155 160

Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg
165 170 175

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys
180 185 190

A-378CIP5.ST25.txt

Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp
195 200 205

Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys
210 215 220

Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp
225 230 235 240

Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
245 250 255

Glu Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro
260 265 270

Ser Phe Ser Pro Thr Pro Gly Phe Thr
275 280

<210> 130
<211> 207
<212> PRT
<213> Rattus rattus

<400> 130

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly
1 5 10 15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp
20 25 30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr
35 40 45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys
50 55 60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val
65 70 75 80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys
85 90 95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys
100 105 110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys
115 120 125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr
130 135 140

A-378CIP5.ST25.txt

Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro
145 150 155 160

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn
165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Ala Gly His Asn
180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr
195 200 205

<210> 131
<211> 227
<212> PRT
<213> Rattus rattus

<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
Page 38

180

185

190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr
 225

<210> 132
 <211> 197
 <212> PRT
 <213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
 20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
 35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
 145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
 165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
 180 185 190

Arg Ala Leu Leu Val
195

<210> 133
<211> 208
<212> PRT
<213> Rattus rattus
<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195 200 205

<210> 134
<211> 224
<212> PRT

A-378CIP5.ST25.txt

<213> Rattus rattus

<400> 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

<210> 135

<211> 205

<212> PRT

<213> Rattus rattus

<400> 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Gly Leu

A-378CIP5.ST25.txt

1

5

10

15

Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
20 25 30

Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
35 40 45

Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
50 55 60

Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
65 70 75 80

Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
85 90 95

Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
100 105 110

Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
115 120 125

His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
130 135 140

Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp
145 150 155 160

Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr
165 170 175

Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp
180 185 190

Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
195 200 205

<210> 136
<211> 191
<212> PRT
<213> Rattus rattus

<400> 136

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
 50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
 65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
 85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
 100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
 115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
 130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
 145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
 165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu
 180 185 190

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<210> 138
 <211> 284
 <212> PRT
 <213> Mus musculus

<400> 138

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala
 1 5 10 15

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe
 20 25 30

Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn
 35 40 45

A-378CIP5.ST25.txt

Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His
50 55 60

Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile
65 70 75 80

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
85 90 95

Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly
100 105 110

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser
115 120 125

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
130 135 140

Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Ala Leu Cys
145 150 155 160

Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu
165 170 175

Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro
180 185 190

Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu
195 200 205

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
210 215 220

Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe
225 230 235 240

Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His
245 250 255

Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
260 265 270

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
275 280

<210> 139
<211> 380
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A-378CIP5.ST25.txt

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
 1 5 10 15

Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
 20 25 30

Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
 35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
 50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
 65 70 75 80

Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
 85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala
 100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe
 115 120 125

Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His
 145 150 155 160

Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile
 165 170 175

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
 180 185 190

Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly
 195 200 205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser
 210 215 220

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn
 225 230 235 240

Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys
 245 250 255

Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu
 260 265 270

A-378CIP5.ST25.txt

Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala
275 280 285

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile
290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr
305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe
325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His
340 345 350

Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile
355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
370 375 380

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<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 141

gtcataatga aggtacttct gggtggtcca

30

<210> 142

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 142

ggaccaccca gtttcattat gacgaagaaa c

31

<210> 143

<211> 31

<212> DNA

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<220>
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<400> 143
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<210> 144
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gtggaccacc caggacgaag aaacctctc 29

<210> 145
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<400> 145
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<210> 146
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<400> 146
cgtttcctcc aaagttcctt cattatgac 29

<210> 147
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<400> 147
gtcataatga aggaactttg gagggaaacg 29

<210> 148
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ggaaacgttt cctgcaaagt acttcatta tg 32

A-378CIP5.ST25.txt

<210> 149

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<400> 149

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27

<210> 151

<211> 27

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<220>

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<400> 151

gtgacatcta ttcccgactt ttgcgtg

27

<210> 152

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 152

caccctgtcg gaagaggcct tcttc

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25

<210> 154

<211> 24

<212> DNA

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A-378CIP5.ST25.txt

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<210> 155
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<400> 155
tgcacgctgc tttccgagag gtca 24

<210> 156
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<400> 156
cctcggaaatc gagcgagcag ctcc 24

<210> 157
<211> 25
<212> DNA
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<220>
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<400> 157
cgatttcgag gtctttctcg ttctc 25

<210> 158
<211> 33
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ccgtgaaaat aagctcgat taactaggaa tgg 33

<210> 159
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<400> 159
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<210> 160
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A-378CIP5.ST25.txt

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<212> DNA
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A-378CIP5.ST25.txt

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38

<210> 167
<211> 38
<212> DNA
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<400> 167
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38

169
<210> 168
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> pAMG22

<400> 168

Met Lys His His His His His His Ala Ser Val Asn Ala Leu Glu
1 5 10 15